IN THE CLAIMS

The following is a copy of Applicant's claims that identifies language being added with underlining ("___") and language being deleted with strikethrough ("———"), as is applicable:

1. (Currently Amended) A method of performing nanopore data analysis with a nanopore device, comprising:

providing a sample including target polynucleotides and non-target polynucleotides;

introducing the sample to the nanopore device;

generating nanopore data points corresponding to each target ~~polymer~~ polynucleotide and each non-target polynucleotide traversing an aperture of the nanopore;

forming a distribution pattern of the nanopore data points, wherein the distribution pattern includes at least one data cluster; and

analyzing a distribution of polynucleotide data points in the distribution pattern ~~to aid in a determination of~~ and determining at least one of the following: phosphorylation state of the target polynucleotides, length diversity among polynucleotides present in a sample, chemical integrity of the target polynucleotides, and a ratio of target polynucleotides to non-target polynucleotides in the sample, and wherein analyzing includes:

analyzing the distribution of target polynucleotide data points within the at least one data cluster; and

comparing the distribution of the target polynucleotide data points between two data clusters to a phosphorylation state standard distribution.

2. (Canceled)

3. (Canceled)

4. (Currently Amended) The method of claim ~~3~~ 1, further comprising:

determining a ratio of phosphorylated target polynucleotide to non-phosphorylated target polynucleotides.

5. (Currently Amended) The method of claim ~~2~~ 1, wherein the target polynucleotides comprise phosphorylated and non-phosphorylated polynucleotides, the method further comprising:

determining a ratio of phosphorylated target polynucleotide to non-phosphorylated target polynucleotides.

6. (Currently Amended) The method of claim ~~2~~ 1, further comprising:

comparing a density distribution of the target polynucleotide data points to a chemical integrity standard density distribution, wherein a change in the density distribution of target polynucleotide data points as compared to the chemical integrity standard density distribution indicates that the chemical integrity of the target polynucleotides in the sample is different than a chemical integrity for which the chemical integrity standard density distribution was prepared.

7. (Original) The method of claim 6, further comprising:

determining the density of target polynucleotide data points in a defined area; and

comparing the density of the target polynucleotide data points to a chemical integrity standard density distribution for the defined area.

8. (Original) The method of claim 6, further comprising:

determining the density of target polynucleotide data points in a defined area;

comparing the density of the target polynucleotide data points to a density of the target polynucleotide data points of at least two other samples including target polynucleotides and non-target polynucleotides; and

ranking the samples based on the density of the target polynucleotide data points.

9. (Original) The method of claim 6, further comprising:

determining a cluster score for the target polynucleotide data points in a defined area; and

comparing the cluster score for the target polynucleotide data points to a cluster score for a chemical integrity standard density distribution for the defined area.

10. (Currently Amended) The method of claim ~~2~~ 1, further comprising:

analyzing the distribution of the non-target polynucleotide data points.

11. (Original) The method of claim 10, wherein distribution of non-target polynucleotide data points outside of the at least one cluster indicates that non-target polynucleotides have a different length than the target polynucleotides.

12. (Original) The method of claim 10, wherein distribution of non-target polynucleotide data points outside of the at least one cluster indicates that the non-target polynucleotides have the same length as the target polynucleotide but the sequence of the non-target polynucleotide and target polynucleotide is not the same.

13. (Original) The method of claim 10, further comprising:

determining a ratio between the target polynucleotide data points and the non-target polynucleotide data points.

14. (Previously Presented) The method of claim 1, wherein the failure of polynucleotide data points to form at least one cluster indicates that the target polynucleotides in the sample represent less than a calibration specified fraction of the total polynucleotides in the sample.

15. (Currently Amended) A system for performing nanopore data analysis, comprising:

a nanopore system including a nanopore device and a nanopore data analysis system, the nanopore device having a structure having an aperture, wherein a polynucleotide traverses the aperture, the nanopore data analysis system operative to:

generate nanopore data points corresponding to each target polynucleotide and each non-target polynucleotide traversing the aperture of the nanopore structure;

form a distribution pattern of the data points; and

analyze a distribution of target polynucleotide data points in the distribution pattern ~~to aid in a determination of~~ and determining at least one of the following: phosphorylation state of the target polynucleotides, length diversity among polynucleotides present in a sample, chemical integrity of the target polynucleotides, and a ratio of target polynucleotides to non-target polynucleotides in the sample, wherein the nanopore data analysis system is further operative to analyze the distribution of the non-target polynucleotide data points, wherein the nanopore data analysis system is further operative to determine a ratio between the target polynucleotide data points and the non-target polynucleotide data points.

16. (Canceled)

17. (Canceled)

18. (Currently Amended) The system of claim 15, wherein the distribution pattern includes at least one data cluster and wherein the nanopore data analysis system is further operative to:

analyze of the distribution of target polynucleotide data points between the two data clusters;

compare the distribution of the target polynucleotide data points between the two data clusters to a phosphorylation state standard distribution; and

determine a ratio of phosphorylated target ~~polynucleotide~~ polynucleotides to non-phosphorylated target polynucleotides.

19. (Previous Presented) The system of claim 15, wherein the nanopore data analysis system is further operative to:

determine a cluster score for the target polynucleotide data points in a defined area; and

compare the cluster score for the target polynucleotide data points to a cluster score for a chemical integrity standard density distribution for the defined area in a distribution of a target polynucleotide standard.

20. (Original) The system of claim 15, wherein the nanopore data analysis system is stored on a computer-readable medium.

21. (Previous Presented) The system of claim 15, further comprising:

means for analyzing the distribution of target polynucleotide data points in the distribution pattern.

22. (Newly Added) A method of performing nanopore data analysis with a nanopore device, comprising:

providing a sample including target polynucleotides and non-target polynucleotides;

introducing the sample to the nanopore device;

generating nanopore data points corresponding to each target polynucleotide and each non-target polynucleotide traversing an aperture of the nanopore;

forming a distribution pattern of the nanopore data points, wherein the distribution pattern includes at least one data cluster;

analyzing a distribution of polynucleotide data points in the distribution pattern and determining at least one of the following: phosphorylation state of the target polynucleotides, length diversity among polynucleotides present in a sample, chemical integrity of the target polynucleotides, a ratio of target polynucleotides to non-target polynucleotides in the sample; and

analyzing includes analyzing the distribution of target polynucleotide data points within the at least one data cluster, wherein the failure of polynucleotide data points to form at least one cluster indicates that the target polynucleotides in the sample represent less than a calibration specified fraction of the total polynucleotides in the sample.

23. (Newly Added) The method of claim 22, further comprising:

comparing the distribution of the target polynucleotide data points between two data clusters to a phosphorylation state standard distribution.

24. (Newly Added) The method of claim 22, further comprising:

determining a ratio of phosphorylated target polynucleotide to non-phosphorylated target polynucleotides.

25. (Newly Added) The method of claim 22, wherein the target polynucleotides comprise phosphorylated and non-phosphorylated polynucleotides, the method further comprising:

determining a ratio of phosphorylated target polynucleotide to non-phosphorylated target polynucleotides.

26. (Newly Added) The method of claim 22, further comprising:

comparing a density distribution of the target polynucleotide data points to a chemical integrity standard density distribution, wherein a change in the density distribution of target polynucleotide data points as compared to the chemical integrity standard density distribution indicates that the chemical integrity of the target polynucleotides in the sample is different than a chemical integrity for which the chemical integrity standard density distribution was prepared.

27. (Newly Added) The method of claim 26, further comprising:

determining the density of target polynucleotide data points in a defined area; and

comparing the density of the target polynucleotide data points to a chemical integrity standard density distribution for the defined area.

28. (Newly Added) The method of claim 26, further comprising:

determining the density of target polynucleotide data points in a defined area;

comparing the density of the target polynucleotide data points to a density of the target polynucleotide data points of at least two other samples including target polynucleotides and non-target polynucleotides; and

ranking the samples based on the density of the target polynucleotide data points.

29. (Newly Added) The method of claim 26, further comprising:

determining a cluster score for the target polynucleotide data points in a defined area; and

comparing the cluster score for the target polynucleotide data points to a cluster score for a chemical integrity standard density distribution for the defined area.

30. (Newly Added) The method of claim 22, further comprising:

analyzing the distribution of the non-target polynucleotide data points.

31. (Newly Added) The method of claim 30, wherein distribution of non-target polynucleotide data points outside of the at least one cluster indicates that non-target polynucleotides have a different length than the target polynucleotides.

32. (Newly Added) The method of claim 30, wherein distribution of non-target polynucleotide data points outside of the at least one cluster indicates that the non-target polynucleotides have the same length as the target polynucleotide but the sequence of the non-target polynucleotide and target polynucleotide is not the same.

33. (Newly Added) The method of claim 30, further comprising:

determining a ratio between the target polynucleotide data points and the non-target polynucleotide data points.

34. (Newly Added) A system for performing nanopore data analysis, comprising:

a nanopore system including a nanopore device and a nanopore data analysis system, the nanopore device having a structure having an aperture, wherein a polynucleotide traverses the aperture, the nanopore data analysis system operative to:

generate nanopore data points corresponding to each target polynucleotide and each non-target polynucleotide traversing the aperture of the nanopore structure;

form a distribution pattern of the data points, wherein the distribution pattern includes at least one data cluster;

analyze a distribution of target polynucleotide data points between the two data clusters;

compare the distribution of the target polynucleotide data points between the two data clusters to a phosphorylation state standard distribution; and

determine a ratio of phosphorylated target polynucleotides to non-phosphorylated target polynucleotides.

35. (Newly Added) A system for performing nanopore data analysis, comprising:

a nanopore system including a nanopore device and a nanopore data analysis system, the nanopore device having a structure having an aperture, wherein a polynucleotide traverses the aperture, the nanopore data analysis system operative to:

generate nanopore data points corresponding to each target polynucleotide and each non-target polynucleotide traversing the aperture of the nanopore structure;

form a distribution pattern of the data points;

analyze a distribution of target polynucleotide data points in the distribution pattern and determining at least one of the following: phosphorylation state of the target polynucleotides, length diversity among polynucleotides present in a sample, chemical integrity of the target polynucleotides, a ratio of target polynucleotides to non-target polynucleotides in the sample;

determine a cluster score for the target polynucleotide data points in a defined area; and

compare the cluster score for the target polynucleotide data points to a cluster score for a chemical integrity standard density distribution for the defined area in a distribution of a target polynucleotide standard.